

SEQUENCE LISTING

<110> Yang, Hongyuan  
National University of Singapore

<120> Triacylglycerol-Deficient Fission Yeast and Its Uses

<130> 040184-000500US

<140> US 10/564,266

<141> 2006-01-09

<150> US 60/485,385

<151> 2003-07-09

<150> WO PCT/SG04/00205

<151> 2004-07-09

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR  
amplification primer PLH1-55

<400> 1

gggttaccac accctatttgc aaca

25

<210> 2

<211> 28

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<223> Description of Artificial Sequence:PCR  
amplification primer PLH1-53

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ccgctcgagg aattgcttga gcagcaac

28

<210> 3

<211> 28

<212> DNA

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28

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<210> 8
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<210> 11
<211> 26
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<210> 12
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ccgctcgagg gtaggttagta tagttaga 28

<210> 13
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      primer in coding region of ura4+

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<400> 13  
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<223> Description of Artificial Sequence:diagnostic PCR primer in coding region of his3+

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<213> Schizosaccharomyces pombe

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<223> diacylglycerol O-acyltransferase (dgat1; GeneDB  
Accession No. SPCC1235.15)

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Ile Ser Lys Asp Ser Arg Arg Asn Val Ser His Trp Leu Gln Ala Leu  
20 25 30  
  
Ala Val Phe Leu His Ser Val Ser Leu Thr Leu Thr Ala Ser Trp Tyr  
35 40 45  
  
Thr Val Leu Trp Ala Phe Leu Pro Phe Trp Pro Phe Leu Ile Val Tyr  
50 55 60  
  
Leu Ile Trp Leu Ile Tyr Asp Asp Gly Phe Val Thr Gly Lys Asp Arg  
65 70 75 80  
  
Gln Lys Arg Trp Leu Arg Asn Ala Pro Pro Tyr Arg Trp Phe Cys His  
85 90 95  
  
Tyr Phe Pro Ile Arg Leu His Lys Thr Thr Glu Leu Asp Ser Glu Lys  
100 105 110  
  
Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Ile Ser Leu Gly Ala  
115 120 125  
  
Phe Gly Gly Phe Ala Ser Glu Gly Ala Asp Phe Ser Lys Leu Phe Pro  
130 135 140  
  
Gly Ile Asn Val Ser Val Leu Thr Leu Asn Ser Asn Phe Tyr Val Pro  
145 150 155 160  
  
Val Tyr Arg Asp Tyr Leu Met Ala Leu Asn Ile Asn Ser Val Ser Lys  
165 170 175  
  
Lys Ser Cys Val Ser Ile Leu Ser Arg Lys Pro Gly Asp Ser Val Leu  
180 185 190  
  
Ile Val Ile Gly Gly Ala Gln Glu Ser Leu Leu Ser Arg Pro Gly Gln  
195 200 205  
  
Asn Asn Leu Val Leu Lys Lys Arg Phe Gly Phe Val Lys Leu Ala Phe  
210 215 220  
  
Leu Thr Gly Ser Ser Leu Val Pro Cys Phe Ala Phe Gly Glu Ser Asp  
225 230 235 240  
  
Ile Phe Glu Gln Val Asp Asn Asn Pro Arg Thr Arg Ile Tyr Lys Phe  
245 250 255

Gln	Glu	Ile	Val	Lys	Lys	Ile	Ala	Gly	Phe	Thr	Val	Pro	Phe	Phe	Tyr
260						265						270			
Gly	Arg	Gly	Leu	Leu	Asn	Lys	Thr	Phe	Gly	Leu	Met	Pro	Trp	Arg	Lys
275						280					285				
Pro	Ile	Asn	Ile	Val	Val	Gly	Glu	Pro	Ile	Asp	Val	Pro	Lys	Lys	Ser
290						295						300			
His	Pro	Thr	Asn	Gln	Glu	Ile	Tyr	Glu	Val	His	Glu	Glu	Tyr	Ile	Arg
305						310				315			320		
Arg	Leu	Glu	Gly	Leu	Trp	Asn	Lys	Tyr	Lys	Asp	Val	Phe	Leu	Pro	Asn
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Arg	Ile	Ser	Glu	Leu	Lys	Leu	Ser	Ala							
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<210> 24  
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 <212> PRT  
 <213> Schizosaccharomyces pombe

<220>  
 <223> phospholipid-diacylglycerol acyltransferase (plhl,  
 GeneDB Accession No. SPBC776.14, Pombe LRO1  
 Homolog 1), Lecithin:cholesterol acyltransferase

<400> 24  
 Met Ala Ser Ser Lys Lys Ser Lys Thr His Lys Lys Lys Glu Val  
 1 5 10 15

Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu  
 20 25 30

Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser  
 35 40 45

Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile  
 50 55 60

Leu Gly Ile Cys Gly Ala Phe Phe Ala Val Gly Asp Asp Asn Ala  
 65 70 75 80

Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser  
 85 90 95

Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe  
 100 105 110

Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly  
 115 120 125

Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser  
 130 135 140

Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu  
 145 150 155 160

Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu  
 165 170 175  
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys  
 180 185 190  
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys  
 195 200 205  
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe  
 210 215 220  
 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala  
 225 230 235 240  
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg  
 245 250 255  
 Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu  
 260 265 270  
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val  
 275 280 285  
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys  
 290 295 300  
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Pro Thr Trp Val Asn  
 305 310 315 320  
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala  
 325 330 335  
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly  
 340 345 350  
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu  
 355 360 365  
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro  
 370 375 380  
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser  
 385 390 395 400  
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp  
 405 410 415  
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp  
 420 425 430  
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala  
 435 440 445  
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp  
 450 455 460  
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile  
 465 470 475 480

Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr  
485 490 495

Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp  
500 505 510

Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr  
515 520 525

Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr  
530 535 540

Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys  
545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu  
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys  
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp  
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn  
610 615 620